



Sequences producing significant alignments:	Score (bits)	E Value
gi 34101278 ref NP_898888.1 hypothetical protein MGC10744 ...	299	3e-80
gi 34101276 ref NP_115730.2 hypothetical protein MGC10744 ...	290	2e-77
gi 47123437 gb AAH70231.1 Unknown (protein for MGC:88213) ...	275	9e-73
gi 27672842 ref XP_213332.1 similar to RIKEN cDNA 1110004B...	255	5e-67
gi 21539609 ref NP_080114.1 RIKEN cDNA 1110004B13 [Mus mus...	253	3e-66
gi 21539635 ref NP_082612.1 RIKEN cDNA 1110004B13 [Mus mus...	215	9e-55
gi 13751660 gb AAK38512.1 DC20 [Homo sapiens]	134	2e-30
gi 47086013 ref NP_998376.1 zgc:77926 [Danio rerio] >gi 41...	133	4e-30
gi 47225380 emb CAG11863.1 unnamed protein product [Tetrao...	118	8e-26
gi 34535000 dbj BAC87177.1 unnamed protein product [Homo s...	57	3e-07
gi 29347399 ref NP_810902.1 conserved hypothetical protein...	35	1.6
gi 32421327 ref XP_331107.1 predicted protein [Neurospora ...	35	1.6
gi 40739337 gb EAA58527.1 hypothetical protein AN6709.2 [A...	35	2.1
gi 15965618 ref NP_385971.1 HYPOTHETICAL TRANSMEMBRANE PRO...	34	3.9
gi 13161475 emb CAC32898.1 cytochrome oxidase I [Aleochara...	33	5.2
gi 21402628 ref NP_658613.1 hypothetical protein predicted...	33	5.2
gi 47564995 ref ZP_00236038.1 membrane protein, putative [...	33	5.2
gi 22298906 ref NP_682153.1 molybdenum cofactor biosynthes...	33	5.2
gi 30022660 ref NP_834291.1 Integral membrane protein [Bac...	33	5.2
gi 18389591 dbj BAB84303.1 NorB homologue [Roseobacter den...	32	12

gi 31980760 ref NP_082619.2	RIKEN cDNA 2810439K08 [Mus mus...]	32	12	
gi 12850533 dbj BAB28760.1	unnamed protein product [Mus mu...]	32	12	
gi 11465549 ref NP_045059.1	unknown [Cyanidium caldarium] ...	32	12	
gi 26324794 dbj BAC26151.1	unnamed protein product [Mus mu...]	32	12	
gi 32398820 emb CAD98530.1	DNA topoisomerase III beta-1, p...	32	12	
gi 26327641 dbj BAC27564.1	unnamed protein product [Mus mu...]	32	12	
gi 26338636 dbj BAC32989.1	unnamed protein product [Mus mu...]	32	12	
gi 34857825 ref XP_218880.2	similar to CG11737-PA [Rattus ...]	32	12	
gi 45199242 ref NP_986271.1	AFR723Cp [Eremotheicum gossypi...]	32	17	
gi 20148896 gb AAM12701.1	cytochrome oxidase subunit I [Co...]	32	17	
gi 23346515 ref NP_694731.1	suppression of tumorigenicity ...	32	17	
gi 6912318 ref NP_036264.1	claudin 8; human CLDN8 gene for...	32	17	
gi 34859740 ref XP_215667.2	similar to Tumorsuppressor St7...	32	17	
gi 34904472 ref NP_913583.1	OSJNBa0086P08.15 [Oryza sativa...]	32	17	
gi 32398745 emb CAD98705.1	hypothetical predicted protein,...	32	17	
gi 20148882 gb AAM12694.1	cytochrome oxidase subunit I [Co...]	31	22	
gi 39581918 emb CAE72880.1	Hypothetical protein CBG20192 [...]	31	22	
gi 17553936 ref NP_497809.1	heavy chain, Unconventional My...	31	22	
gi 48731822 ref ZP_00265566.1	COG2375: Siderophore-interac...	31	22	
gi 15805226 ref NP_293914.1	conserved hypothetical protein...	31	22	
gi 6679134 ref NP_032763.1	neuropilin; Neuropilin-1 [Mus m...]	31	22	
gi 2407643 gb AAC53345.1	neuropilin [Rattus norvegicus]	31	22	
gi 20148886 gb AAM12696.1	cytochrome oxidase subunit I [Co...]	31	22	
gi 37805305 gb AAH60129.1	Neuropilin [Mus musculus]	31	22	
gi 48123803 ref XP_393257.1	similar to ENSANGP00000020727 ...	31	22	
gi 26023947 ref NP_659566.1	neuropilin [Rattus norvegicus]...	31	22	
gi 42783762 ref NP_981009.1	membrane protein, putative [Ba...]	31	30	
gi 13162192 emb CAC33080.1	cytochrome oxidase I [Aleochara...]	31	30	
gi 32564324 ref NP_499385.2	membrane Calcium ATPase, Sarco...	31	30	
gi 16081573 ref NP_393930.1	sugar transport protein relate...	31	30	
gi 32698592 ref NP_872507.1	p74 [Adoxophyes orana granulov...]	31	30	
gi 46111503 ref XP_382809.1	hypothetical protein FG02633.1...	31	30	
gi 16126505 ref NP_421069.1	phosphorylase family protein [...]	31	30	
gi 29135128 ref NP_803758.1	ORF192 [Pseudomonas phage phiK...	31	30	
gi 39591819 emb CAE71397.1	Hypothetical protein CBG18305 [...]	31	30	
gi 18478322 gb AAL73125.1	neutral endopeptidase-like prote...	30	40	
gi 2133376 pir S58192	hypothetical protein - Leishmania me...	30	40	
gi 6118323 gb AAF04069.1	cytochrome oxidase I [Xylosandrus...]	30	40	
gi 24762656 ref NP_611923.1	CG13582-PA [Drosophila melanog...	30	40	
gi 40254452 ref NP_003864.2	neuropilin 1 [Homo sapiens] >g...	30	40	
gi 9297107 sp O14786 NRP1_HUMAN	Neuropilin-1 precursor (Vas...	30	40	
gi 11934946 gb AAG41896.1	neuropilin-1 [Homo sapiens]	30	40	
gi 32414281 ref XP_327620.1	hypothetical protein [Neurospo...	30	40	
gi 15021676 gb AAK77867.1	neuropilin-1 [Ovis aries]	30	40	
gi 6118331 gb AAF04077.1	cytochrome oxidase I [Xylosandrus...]	30	40	
gi 31324910 ref NP_852164.1	cytochrome c oxidase subunit I...	30	40	
gi 2407641 gb AAC51759.1	neuropilin [Homo sapiens]	30	40	
gi 23098373 ref NP_691839.1	hypothetical protein OB0918 [O...	30	54	
gi 41146565 ref XP_371664.1	KIAA1257 protein [Homo sapiens]	30	54	
gi 24270835 gb AAH38736.1	Unknown (protein for IMAGE:52679...	30	54	
gi 21740283 emb CAD39151.1	hypothetical protein [Homo sapi...	30	54	
gi 15615500 ref NP_243804.1	BH2938~unknown conserved prote...	30	54	

gi 6118322 gb AAF04068.1 cytochrome oxidase I [Xyleborinus...	30	54	
gi 31377711 ref NP_075069.2 hypothetical protein FLJ22104 ...	30	54	L
gi 21594958 gb AAH31632.1 KIAA1257 protein [Homo sapiens]	30	54	L
gi 27375449 ref NP_766978.1 Alpha-methylacyl-CoA racemase ...	30	54	L
gi 6330918 dbj BAA86571.1 KIAA1257 protein [Homo sapiens]	30	54	L
gi 19704318 ref NP_603880.1 Hypothetical protein [Fusobact...	30	54	
gi 17987441 ref NP_540075.1 NADH-QUINONE OXIDOREDUCTASE CH...	29	73	
gi 7519161 pir H71023 hypothetical protein PH1485 - Pyroco...	29	73	
gi 48783379 ref ZP_00279831.1 COG0477: Permeases of the ma...	29	73	
gi 15896540 ref NP_349889.1 Probable cation efflux pump (m...	29	73	
gi 23501689 ref NP_697816.1 NADH dehydrogenase I, A subuni...	29	73	
gi 16588684 gb AAL26868.1 anion transporter/exchanger-8 [H...	29	73	L
gi 48825325 ref ZP_00286583.1 COG3711: Transcriptional ant...	29	73	
gi 15601302 ref NP_232933.1 conserved hypothetical protein...	29	73	
gi 7322060 gb AAA31968.2 ATPase subunit 6 [Naegleria fowleri]	29	73	
gi 47605712 sp Q8MIB6 EFC1 PANTR ERV-F(c)1 provirus ancestr...	29	73	
gi 16418457 ref NP_443193.1 solute carrier family 26, memb...	29	73	L
gi 19263998 gb AAH25408.1 Solute carrier family 26, member...	29	73	L
gi 23098187 ref NP_691653.1 hypothetical protein OB0732 [O...	29	73	
gi 15810667 gb AAL08583.1 FGF2-associated protein GAFAl [H...	29	73	
gi 9453728 emb CAB99354.1 bA48209.4 (Novel sulphate transp...	29	73	L
gi 47219823 emb CAG03450.1 unnamed protein product [Tetrao...	29	73	
gi 20336285 ref NP_619732.1 solute carrier family 26, memb...	29	73	
gi 40742890 gb EAA62080.1 hypothetical protein AN7500.2 [A...	29	73	
gi 41724135 ref ZP_00151001.1 COG1742: Uncharacterized con...	29	73	
gi 6562165 emb CAB62533.1 hypothetical protein [Homo sapiens]	29	73	L
gi 37546246 ref XP_066621.3 similar to envelope protein [H...	29	73	L
gi 46435250 gb EAK94636.1 hypothetical protein Ca019.11163...	29	73	

Alignments

Get selected sequences
 Select all
 Deselect all

>gi|34101278|ref|NP_898888.1| L hypothetical protein MGC10744 isoform 2 [Homo sa
 gi|37182173|gb|AAQ88889.1| GRVS638 [Homo sapiens]
 Length = 140

Score = 299 bits (699), Expect = 3e-80
 Identities = 114/141 (80%), Positives = 118/141 (83%), Gaps = 15/141 (10%)

Query: 1 MGRVSGLVPSRFLTLTAHLN--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54
 MGRVSGLVPSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDIQLV SV

Sbjct: 1 MGRVSGLVPSRFLTLAHLVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSV 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLSISIGM-CSASV-MSFFIFERWECTTYWYIW-FCS- 107
 TLGLFA GFLSGVSM STQLSISIG CSASV +SFFIFERWECTTYWYI+ FCS

Sbjct: 60 TLGLFAVELAGFLSGVSMFNSTQLSISIGAHCSASVALSFFIFERWECTTYWYIFVFCSA 119

Query: 108 MPAVTEMATW-TVFGLKKKPF 127
 +PAVTEMA + TVFGLKKKPF

Sbjct: 120 LPAVTEMALFVTVFGLKKKPF 140

□>gi|34101276|ref|NP_115730.2| L hypothetical protein MGC10744 isoform 1 [Homo sa
Length = 146

Score = 290 bits (677), Expect = 2e-77
Identities = 113/147 (76%), Positives = 117/147 (79%), Gaps = 21/147 (14%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQ-----L 50
MGRVSGLVPNSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDI L
Sbjct: 1 MGRVSGLVPNSRFLTLAHLVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIHPLPLCRL 59

Query: 51 V--WSVTLGLFA--WMGFLSGVSMM-STQLSISGM-CSASV-MSFFIFERWECTTYWYI 103
V SVTLGLFA GFLSGVSM STQLSISIG CSASV +SFFIFERWECTTYWYI
Sbjct: 60 VAALSVTGLFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYI 119

Query: 104 W-FCS-MPAVTEMATW-TVFGLKKPF 127
+ FCS +PAVTEMA + TVFGLKKPF
Sbjct: 120 FVFCALPAVTEMALFVTVFGLKKPF 146

□>gi|47123437|gb|AAH70231.1| Unknown (protein for MGC:88213) [Homo sapiens]
Length = 139

Score = 275 bits (641), Expect = 9e-73
Identities = 108/145 (74%), Positives = 112/145 (77%), Gaps = 24/145 (16%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQ-----L 50
MGRVSGLVPNSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDI L
Sbjct: 1 MGRVSGLVPNSRFLTLAHLVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIHPLPLCRL 59

Query: 51 V--WSVTLGLFA--WMGFLSGVSMM-STQLSISGM-CSASV-MSFFIFERWECTTYWYI 103
V SVTLGLFA GFLSGVSM STQLSISIG CSASV +SFFIFERWECTTY
Sbjct: 60 VAALSVTGLFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTY-- 116

Query: 104 WFCMSMPAVTEMATW-TVFGLKKPF 127
C+PAVTEMA + TVFGLKKPF
Sbjct: 117 --CALPAVTEMALFVTVFGLKKPF 139

□>gi|27672842|ref|XP_213332.1| L similar to RIKEN cDNA 1110004B13 [Rattus norvegi
Length = 140

Score = 255 bits (596), Expect = 5e-67
Identities = 103/141 (73%), Positives = 111/141 (78%), Gaps = 15/141 (10%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--TLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54
MGR+SGLVPNSRFLTL AHL I TL SR+SNIQACLPL FTPEEY+KQD QLV +
Sbjct: 1 MGRISGLVPNSRFLTLAHLVIVITL-FWSRESNIQACLPLKFTPEEYEKQDNQLVAALCL 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLSISGM-CSASV-MSFFIFERWECTTYWYIW-FCS- 107
TLGLFA GFLSGVSM STQLS+SI CSASV +SFFIFERWECTTYWYI+ FCS
Sbjct: 60 TLGLFAVELAGFLSGVSMFNSTQSLLSIAAHCSASVALSFFIFERWECTTYWYIFAFCSA 119

Query: 108 MPAVTEMATW-TVFGLKKPF 127
PAVTE A + VFGLKKPF
Sbjct: 120 FPAVTETALFIAVFGLKKPF 140

□ >gi|21539609|ref|NP_080114.1| L RIKEN cDNA 1110004B13 [Mus musculus]
 gi|12834053|dbj|BAB22768.1| L unnamed protein product [Mus musculus]
 Length = 140

Score = 253 bits (590), Expect = 3e-66
 Identities = 102/141 (72%), Positives = 111/141 (78%), Gaps = 15/141 (10%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54
 MGR+SGLVPSRFLTL AHL ITL SR+SNIQACLPL FTPEEY+KQD QLV +
 Sbjct: 1 MGRISGLVPNSRFLTLAAHVVVITL-FWSRESNIQACLPLKFTPEEYEKQDNQLVAALCL 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLISIGM-CSASV-MSFFIFERWECTTYWYIW-FCS- 107
 TLGLFA GFLSGVSM STQL+SI CSASV +SFF+FERWECTTYWYI+ FCS
 Sbjct: 60 TLGLFAVELAGFLSGVSMFNSTQSLISIAAHCSASVALSFFVFERWECTTYWYIIFTFC 119

Query: 108 MPAVTEMATW-TVFGKKKPF 127
 PAVTE A + VFGLKKKPF
 Sbjct: 120 FPAVTETALFIAVFGKKKPF 140

□ >gi|21539635|ref|NP_082612.1| L RIKEN cDNA 1110004B13 [Mus musculus]
 gi|12850002|dbj|BAB28560.1| L unnamed protein product [Mus musculus]
 Length = 143

Score = 215 bits (500), Expect = 9e-55
 Identities = 85/118 (72%), Positives = 93/118 (78%), Gaps = 13/118 (11%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQLV--WSV 54
 MGR+SGLVPSRFLTL AHL ITL SR+SNIQACLPL FTPEEY+KQD QLV +
 Sbjct: 1 MGRISGLVPNSRFLTLAAHVVVITL-FWSRESNIQACLPLKFTPEEYEKQDNQLVAALCL 59

Query: 55 TLGLFA--WMGFLSGVSMM-STQLISIGM-CSASV-MSFFIFERWECTTYWYIW-FC 106
 TLGLFA GFLS VSM STQL+SI CSASV +SFF+FERWECTTYWYI+ FC
 Sbjct: 60 TLGLFAVELAGFLSRVSMFNSTQSLISIAAHCSASVALSFFVFERWECTTYWYIIFTFC 117

□ >gi|13751660|gb|AAK38512.1| L DC20 [Homo sapiens]
 Length = 141

Score = 134 bits (309), Expect = 2e-30
 Identities = 52/69 (75%), Positives = 52/69 (75%), Gaps = 13/69 (18%)

Query: 1 MGRVSGLVPNSRFLTLTAHNL--ITLD--SRDSNIQACLPLTFTPEEYDKQDIQ-----L 50
 MGRVSGLVPNSRFLTL AHL ITL SRDSNIQACLPLTFTPEEYDKQDI L
 Sbjct: 1 MGRVSGLVPNSRFLTLAAHVVVITL-FWSRDSNIQACLPLTFTPEEYDKQDIHPLPLCRL 59

Query: 51 V--WSVTLG 57
 V SVTLG
 Sbjct: 60 VAALSVTLG 68

□ >gi|47086013|ref|NP_998376.1| L zgc:77926 [Danio rerio]
 gi|41351480|gb|AAH65897.1| L Zgc:77926 [Danio rerio]

Length = 135

Score = 133 bits (307), Expect = 4e-30
 Identities = 68/123 (55%), Positives = 83/123 (67%), Gaps = 18/123 (14%)

Query: 7 LVPSRFLTLTAHLNITLD---SRDSNIQACLPLTFTPEEYDKQDIQL--VWSVTLGLF-- 59
 LVP+RFLTLTAHL I + SRD+NIQ+CLPL FT +Y +D +L SVTL LF

Sbjct: 7 LVPARFLTLTAHLVIIITIFWSRDNNIQSCLPLEFTEDQYRTEDTRLTVALSVTLALFVL 66

Query: 60 --AWMGFLSGVSM-MTQSLIS-IGMCSASV-MSFFIFERWECTTYWYIWF--CSM-PAV 111
 A GFLSGVSM S Q+L+S I SA V +SFF+F +W C TYW I F CS+ PAV

Sbjct: 67 ELA--GFLSGVSMFNSNQALLSLITHSSACVCLSFFVHQWPCWTYWII-FSICSVFPAV 123

Query: 112 TEM 114

E+

Sbjct: 124 VEL 126

>gi|47225380|emb|CAG11863.1| unnamed protein product [Tetraodon nigroviridis]

Length = 180

Score = 118 bits (273), Expect = 8e-26
 Identities = 58/110 (52%), Positives = 78/110 (70%), Gaps = 10/110 (9%)

Query: 4 VSGLVPSRFLTLTAHLNITLD---SRDSNIQACLPLTFTPEEYDKQDIQLV--WSVTLGL 58
 VS LVP+RFLT+ AHL I + SR++N++A LPL FT E+YD +D +LV +VT+G+

Sbjct: 4 VSSLVPARFLTIIAHLVIVITIFWSRENNVRAGLPLDFTQEYDSEDRKLVIALAVTIGM 63

Query: 59 FA--WMGFLSGVSMMS-TQSLISIGM-CSASV-MSFFIFERWECTTYWYI 103

FA GF SGVSM + +Q L+S G SASV + FF+FE+WEC YW+I

Sbjct: 64 FAIELAGFFSGVSMFNCQGLLSTGTHASASVALLFFLFEQWECDIYWWI 113

>gi|34535000|dbj|BAC87177.1| unnamed protein product [Homo sapiens]

Length = 163

Score = 57.5 bits (128), Expect = 3e-07
 Identities = 21/25 (84%), Positives = 21/25 (84%), Gaps = 2/25 (8%)

Query: 1 MGRVSGLVPSRFLTLTAHL--NITL 23

MGRVSGLVPSRFLTL AHL ITL

Sbjct: 1 MGRVSGLVPSRFLTLAHLVVVITL 25

>gi|29347399|ref|NP_810902.1| conserved hypothetical protein [Bacteroides thetai VPI-5482]

gi|29339299|gb|AAO77096.1| conserved hypothetical protein [Bacteroides thetaiota VPI-5482]

Length = 360

Score = 35.0 bits (75), Expect = 1.6

Identities = 17/42 (40%), Positives = 21/42 (50%), Gaps = 21/42 (50%)

Query: 36 LTFTPEEYDKQDIQLVWSVTLGL-----FAWMG 63

LTFT EYD++DI+ LGL FA+MG

Sbjct: 198 LTFT-EEYDERDIE-----LGLIKHIEKFLVEMGAGFAFMG 232

□ >gi|32421327|ref|XP_331107.1| predicted protein [Neurospora crassa]
gi|28921209|gb|EAA30521.1| predicted protein [Neurospora crassa]
Length = 155

Score = 35.0 bits (75), Expect = 1.6
Identities = 10/13 (76%), Positives = 10/13 (76%), Gaps = 2/13 (15%)

Query: 108 MPAVTEMATWTVF 120
MP TEM TWTVF
Sbjct: 130 MP--TEMPTWTVF 140

□ >gi|40739337|gb|EAA58527.1| hypothetical protein AN6709.2 [Aspergillus nidulans]
Length = 1999

Score = 34.6 bits (74), Expect = 2.1
Identities = 13/24 (54%), Positives = 17/24 (70%), Gaps = 2/24 (8%)

Query: 61 WMGFLSGVS--MMSTQSLISIGMC 82
WM FLSG+S M TQ+L +I +C
Sbjct: 1075 WMSFLSGLSAPMQDTQNLKTIKLC 1098

□ >gi|15965618|ref|NP_385971.1| HYPOTHETICAL TRANSMEMBRANE PROTEIN [Sinorhizobium
gi|15074799|emb|CAC46444.1| HYPOTHETICAL TRANSMEMBRANE PROTEIN [Sinorhizobium mel
Length = 302

Score = 33.7 bits (72), Expect = 3.9
Identities = 14/26 (53%), Positives = 17/26 (65%), Gaps = 9/26 (34%)

Query: 50 LVWSVTLGL--FA----WMGFLSGV 68
L+WSVTLG+ FA WM L+GV
Sbjct: 247 LLWSVTLGVVFFAETPDRWM--LAGV 270

□ >gi|13161475|emb|CAC32898.1| cytochrome oxidase I [Aleochara cf. chrysorrhoea]
Length = 457

Score = 33.3 bits (71), Expect = 5.2
Identities = 16/31 (51%), Positives = 16/31 (51%), Gaps = 11/31 (35%)

Query: 68 VSMMSTQSLISIGMCSASVMS--FFIFERWE 96
VS M SLIS M MS FFIF WE
Sbjct: 397 VSSMG--SLIS--M----MSIIFIFIWE 418

□ >gi|21402628|ref|NP_658613.1| hypothetical protein predicted by GeneMark [Bacill
A2012]
gi|30264655|ref|NP_847032.1| membrane protein, putative [Bacillus anthracis str.
gi|47530125|ref|YP_021474.1| membrane protein, putative [Bacillus anthracis str.
gi|30259330|gb|AAP28518.1| membrane protein, putative [Bacillus anthracis str. Am

gi|47505273|gb|AAT33949.1| membrane protein, putative [Bacillus anthracis str. Am
Length = 210

Score = 33.3 bits (71), Expect = 5.2
Identities = 10/13 (76%), Positives = 12/13 (92%)

Query: 75 SLISIGMCSASVM 87
S+I IGMCSA+VM
Sbjct: 36 SIIIIIGMCSAAVM 48

gi|47564995|ref|ZP_00236038.1| membrane protein, putative [Bacillus cereus G924
gi|47557781|gb|EAL16106.1| membrane protein, putative [Bacillus cereus G9241]
Length = 210

Score = 33.3 bits (71), Expect = 5.2
Identities = 10/13 (76%), Positives = 12/13 (92%)

Query: 75 SLISIGMCSASVM 87
S+I IGMCSA+VM
Sbjct: 36 SIIIIIGMCSAAVM 48

gi|22298906|ref|NP_682153.1| molybdenum cofactor biosynthesis protein A [Thermo
elongatus BP-1]
gi|22295087|dbj|BAC08915.1| molybdenum cofactor biosynthesis protein A [Thermosyn
elongatus BP-1]
Length = 332

Score = 33.3 bits (71), Expect = 5.2
Identities = 18/37 (48%), Positives = 19/37 (51%), Gaps = 14/37 (37%)

Query: 7 LVPSRFLTLTAH----LNITLDSRDSNIQACLPLTF 38
LVP FL L AH LNI+LDS D P TF
Sbjct: 120 LVP--FLPLLAHYGVRRLNISLDSL-----PQTF 147

gi|30022660|ref|NP_834291.1| Integral membrane protein [Bacillus cereus ATCC 14
gi|29898218|gb|AAP11492.1| Integral membrane protein [Bacillus cereus ATCC 14579]
Length = 210

Score = 33.3 bits (71), Expect = 5.2
Identities = 10/13 (76%), Positives = 12/13 (92%)

Query: 75 SLISIGMCSASVM 87
S+I IGMCSA+VM
Sbjct: 36 SIIIIIGMCSAAVM 48

gi|18389591|dbj|BAB84303.1| NorB homologue [Roseobacter denitrificans]
Length = 434

Score = 32.0 bits (68), Expect = 12
Identities = 21/56 (37%), Positives = 25/56 (44%), Gaps = 21/56 (37%)

Query: 43 YDKQDIQLV-WSVTLGLFA-----WM----GFLSG-----VSMMSTQSLI 77
 Y Q I LV ++V LGLFA W+ FLS V M+ T SLI
 Sbjct: 3 YQSQSIALVYFAVALGLFAIQVSGGLLGWIYVSPNFLSEILPFNIVRMLHTNSLI 58

□ >gi|31980760|ref|NP_082619.2| L RIKEN cDNA 2810439K08 [Mus musculus]
 gi|26324358|dbj|BAC25933.1| L unnamed protein product [Mus musculus]
 Length = 458

Score = 32.0 bits (68), Expect = 12
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 63 GFLSGVSM---STQSLISIGM 81
 GFL+GVSMM ST +I M
 Sbjct: 334 GFLAGVSMFYKST---TISM 351

□ >gi|12850533|dbj|BAB28760.1| L unnamed protein product [Mus musculus]
 gi|15192728|gb|AAK84685.1| L putative transmembrane protein [Mus musculus]
 gi|23273857|gb|AAH33279.1| L RIKEN cDNA 2810439K08 [Mus musculus]
 gi|29748020|gb|AAH50931.1| L RIKEN cDNA 2810439K08 [Mus musculus]
 Length = 458

Score = 32.0 bits (68), Expect = 12
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 63 GFLSGVSM---STQSLISIGM 81
 GFL+GVSMM ST +I M
 Sbjct: 334 GFLAGVSMFYKST---TISM 351

□ >gi|11465549|ref|NP_045059.1| unknown [Cyanidium caldarium]
 gi|6136624|sp|O19887|YC53_CYACA Hypothetical 28.1 kDa protein ycf53
 gi|7484284|pir||T11955 hypothetical protein ORF237 - red alga (Cyanidium caldarium)
 chloroplast
 gi|2465773|gb|AAB82702.1| unknown [Cyanidium caldarium]
 Length = 237

Score = 32.0 bits (68), Expect = 12
 Identities = 15/31 (48%), Positives = 18/31 (58%), Gaps = 10/31 (32%)

Query: 1 MGRVSGLVPSRFLTLTAHLNITLDSRDSNIQ 31
 M R+ RF++L LN LDS DSNIQ
 Sbjct: 1 MNRI-----RFISLI--LN--LDSCDSNIQ 21

□ >gi|26324794|dbj|BAC26151.1| L unnamed protein product [Mus musculus]
 Length = 458

Score = 32.0 bits (68), Expect = 12
 Identities = 12/22 (54%), Positives = 14/22 (63%), Gaps = 7/22 (31%)

Query: 63 GFLSGVSM---STQSLISIGM 81